STIC Search Report
Biotech-Chem Library

USPTO

STIC Database Tracking Number: 102806

TO: **Minh-Tam Davis**
Location: **CM1/8A01&8E12**
Art Unit: **1642**
Sept 6 , **2003**

Case Serial Number: **09/700700**

From: **P. Sheppard**
Location: **CM1-1E03**
Phone: **(703) 308-4499**

sheppard@uspto.gov

Search Notes

From: Chan, Christina
Sent: Saturday, August 30, 2003 9:39 AM
To: Davis, Minh-Tam; STIC-Biotech/ChemLib
Subject: RE: Rush search request for 09/700700

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
308-3973
CM-1, 9B19

-----Original Message-----
From: Davis, Minh-Tam
Sent: Friday, August 29, 2003 10:49 AM
T : Chan, Christina
Subject: Rush search request for 09/700700

1) Please search SEQ ID NO:335 in the following parent cases of 09/439313 for priority date determination.

09439313 <snquery.pl?APPL_ID=09439313>
is a continuation in part of 09352616 <snquery.pl?APPL_ID=09352616>
Which is a continuation in part of 09288946 <snquery.pl?APPL_ID=09288946>
Which is a continuation in part of 09232149 <snquery.pl?APPL_ID=09232149>
Which is a continuation in part of 09159812 <snquery.pl?APPL_ID=09159812>
Which is a continuation in part of 09115453 <snquery.pl?APPL_ID=09115453>
Which is a continuation in part of 09030607 <snquery.pl?APPL_ID=09030607>
Which is a continuation in part of 09020956 <snquery.pl?APPL_ID=09020956>
Which is a continuation in part of 08904804 <snquery.pl?APPL_ID=08904804>
Which is a continuation in part of 08806099 <snquery.pl?APPL_ID=08806099>

1) Please search SEQ ID NO:1 of the instant application against the sequences of 20030022275 (or US 6617129) and 60/051080

Thank you.

(MINH TAM DAVIS)

ART UNIT 1642, ROOM 8A01, MB 8E12

305-2008

Point of Contact
P. Sheppard
Telephone number: (703) 308-4499

Searcher:_____	TYPE OF SEARCH:	VENDOR/COST (where applic.)
Phone:_____	NA Sequences:_____	STN:_____
Location:_____	AA Sequences:_____	DIALOG:_____
Date Picked Up:_____	Structures:_____	Questel/Orbit:_____
Date Completed: 9/6/03	Bibliographic:_____	DRLink:_____
Searcher Prep/Review:_____	Litigation:_____	Lexis/Nexis:_____
Clerical:_____	Full text:_____	Sequence Sys.:_____
Online time:_____	Patent Family:_____	WWW/Internet:_____
	Other:_____	Other (specify):_____

```
> O <
O | O   IntelliGenetics
> O <
```

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file 439313-335X1ist.res made by spaula on Wed 3 Sep 103 16:22:11-PDT.

Query sequence being compared:US-09-439-313-335 (1-2984)
Number of sequences searched: 2159
Number of scores above cutoff: 2159

Results of the initial comparison of US-09-439-313-335 (1-2984) with:

```
File : 6261562.seq
File : 6262245.seq
File : 6395278.seq
File : 6465611.seq
File : 6613872.seq
File : US0806099.seq
File : US08904804.seq
File : US09115453B.seq
File : US09288946.seq
```

Similarity matrix	Unitary	K-tuple	4
Mismatch penalty	1	Joining penalty	30
Gap penalty	1.00	Window size	500
Gap size penalty	0.33		
Cutoff score	0		
Randomization group	0		

SEARCH STATISTICS

| Scores: | Mean | Median | Standard Deviation |
| | 46 | 39 | 112.72 |

Times: CPU   Total Elapsed
              00:00:13.04   00:00:14.00

Number of residues: 1042365
Number of sequences searched: 2159
Number of scores above cutoff: 2159

The scores below are sorted by initial score.
Significance is calculated based on initial score.

3 100% identical sequences to the query sequence were found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. US-09-352-616A-3	Sequence 335, Application	317	310	311	26.07	0
2. US-09-232-149A-3	Sequence 335, Application	2984	278	278	26.07	0
3. US-09-288-946-33	Sequence 335, Application	2984	278	278	26.07	0

The list of other best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 2 standard deviations above mean ****					
4. US-09-352-616A-4	Sequence 434, Application	484	358	483	2.77	0
5. US-09-352-616A-4	Sequence 453, Application	317	310	311	2.34	0
6. US-09-020-956-11	Sequence 115, Application	366	278	364	2.06	0
7. US-09-030-607-11	Sequence 115, Application	366	278	364	2.06	0
8. US-09-352-616A-1	Sequence 115, Application	366	278	364	2.06	0
9. US-09-232-149A-1	Sequence 115, Application	366	278	364	2.06	0
10. US-09-159-812-11	Sequence 115, Application	366	278	364	2.06	0
11. US-09-115-453-11	Sequence 115, Application	366	278	364	2.06	0
12. US-09-288-946-11	Sequence 115, Application	366	278	364	2.06	0
	**** 1 standard deviation above mean ****					
13. US-09-030-607-20	Sequence 207, Application	332	253	318	1.84	0
14. US-09-352-616A-2	Sequence 207, Application	332	253	318	1.84	0
15. US-09-232-149A-2	Sequence 207, Application	332	253	318	1.84	0
16. US-09-159-812-20	Sequence 207, Application	332	253	318	1.84	0
17. US-09-115-453-20	Sequence 207, Application	332	253	318	1.84	0
18. US-09-288-946-20	Sequence 207, Application	332	253	318	1.84	0
19. US-09-352-616A-2	Sequence 295, Application	305	215	303	1.50	0
20. US-09-232-149A-2	Sequence 295, Application	305	215	303	1.50	0
21. US-09-159-812-29	Sequence 295, Application	305	215	303	1.50	0
22. US-09-288-946-29	Sequence 295, Application	305	215	303	1.50	0
	**** 0 standard deviation from mean ****					
23. US-09-030-607-21	Sequence 216, Application	260	156	232	0.98	0
24. US-09-352-616A-2	Sequence 216, Application	260	156	232	0.98	0
25. US-09-232-149A-2	Sequence 216, Application	260	156	232	0.98	0
26. US-09-159-812-21	Sequence 216, Application	260	156	232	0.98	0
27. US-09-115-453-21	Sequence 216, Application	260	156	232	0.98	0
28. US-09-288-946-21	Sequence 216, Application	260	156	232	0.98	0
29. US-09-020-956-53	Sequence 53, Application	484	108	215	0.55	0
30. US-09-030-607-53	Sequence 53, Application	484	108	215	0.55	0

1. US-09-439-313-335 (1-2984)
   US-09-352-616A-3 Sequence 335, Application US/0935261GA

Sequence 335, Application US/0935261GA

PARAMETERS

```
         0    1326  1658  1989  2321  2652  2984
SCORE  0 |---332---663---995---1326---1658---1989---2321---2652---2984|
STDEV    1    3    5    6    8
```

```
Patent No. 6395278
GENERAL INFORMATION:
 APPLICANT:  Dillon, Davin C.
 APPLICANT:  Harlocker, Susan Louise
 APPLICANT:  Jiang, Yuqui
 APPLICANT:  Xu, Jiangchun
 APPLICANT:  Mitcham, Jennifer Lynn
 TITLE OF INVENTION:  COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
 TITLE OF INVENTION:  OF PROSTATE CANCER AND METHODS FOR THEIR USE
 FILE REFERENCE:  210121.427C8
 CURRENT APPLICATION NUMBER: US/09/352,616A
 CURRENT FILING DATE:  1999-07-13
 NUMBER OF SEQ ID NOS:  472
 SOFTWARE:  FastSEQ for Windows Version 3.0
SEQ ID NO 335
  LENGTH: 2984
  TYPE: DNA
  ORGANISM: Homo sapien

Initial Score     =    2984  Optimized Score  =    2984  Significance = 26.07
Residue Identity =    100%  Matches          =    2984  Mismatches   =     0
Gaps              =       0  Conservative Substitutions             =     0

     X       10        20        30        40        50        60        70
     ATCCCTCCTTCCCCACTCTCCTTTCCAGAAGGCACTTGGGGTCTTATCTGTTGGACTCTGAAAACACTTCAG
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     ATCCCTCCTTCCCCACTCTCCTTTCCAGAAGGCACTTGGGGTCTTATCTGTTGGACTCTGAAAACACTTCAG
     X       10        20        30        40        50        60        70

             80        90       100       110       120       130       140
     GCGCCCTTCCAAGGCTTCCCCAAACCCCTAAGCAGCCGCAGAAGCGCTCCCGAGCTGCCTTCTCCCACACTC
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     GCGCCCTTCCAAGGCTTCCCCAAACCCCTAAGCAGCCGCAGAAGCGCTCCCGAGCTGCCTTCTCCCACACTC
             80        90       100       110       120       130       140

            150       160       170       180       190       200       210
     AGGTGATCGAGTTGGAGAGGAAGTTCAGCCATCAGAAGTACCTGTCGGCCCCTGAACGGGCCCACCTGGCCA
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     AGGTGATCGAGTTGGAGAGGAAGTTCAGCCATCAGAAGTACCTGTCGGCCCCTGAACGGGCCCACCTGGCCA
            150       160       170       180       190       200       210

        220       230       240       250       260       270       280
     AGAACCTCAAGCTCACGGAGACCCAAGTGAAGATATGGTTCCAGAACAGACGCTATAAGACTAAGCGAAAGC
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     AGAACCTCAAGCTCACGGAGACCCAAGTGAAGATATGGTTCCAGAACAGACGCTATAAGACTAAGCGAAAGC
        220       230       240       250       260       270       280

   290       300       310       320       330       340       350       360
     AGCTCTCCTCGGAGCTGGGAGACTTGGAGAAGCACTCCTCTTTGCCGGCCCTGAAAGAGGAGGCCTTCTCCC
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     AGCTCTCCTCGGAGCTGGGAGACTTGGAGAAGCACTCCTCTTTGCCGGCCCTGAAAGAGGAGGCCTTCTCCC
   290       300       310       320       330       340       350       360

             370       380       390       400       410       420       430
     GGGCCTCCCTGGTCTCCGTGTATAACAGCTATCCTTACTACCCATACCTGTACTGCGTGGGCAGCTGGAGCC
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     GGGCCTCCCTGGTCTCCGTGTATAACAGCTATCCTTACTACCCATACCTGTACTGCGTGGGCAGCTGGAGCC
             370       380       390       400       410       420       430

          440       450       460       470       480       490       500
     CAGCTTTTTGGTAATGCCAGCTCAGGTGACAACCATTATGATCAAAAACTGCCTTCCCCAGGGTGTCTCTAT
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     CAGCTTTTTGGTAATGCCAGCTCAGGTGACAACCATTATGATCAAAAACTGCCTTCCCCAGGGTGTCTCTAT
          440       450       460       470       480       490       500

       510       520       530       540       550       560       570
     GAAAAGCACAAGGGGCCAAGGTCAGGGAGCAAGAGGTGTGCACACCAAAGCTATTGGAGATTTGCGTGGAAA
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     GAAAAGCACAAGGGGCCAAGGTCAGGGAGCAAGAGGTGTGCACACCAAAGCTATTGGAGATTTGCGTGGAAA
       510       520       530       540       550       560       570

     580       590       600       610       620       630       640
     TCTCASATTCTTCACTGGTGAGACAATGAAACAACAGAGACAGTGAAAGTTTTAATACCTAAGTCATTCCCC
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     TCTCASATTCTTCACTGGTGAGACAATGAAACAACAGAGACAGTGAAAGTTTTAATACCTAAGTCATTCCCC
     580       590       600       610       620       630       640

   650       660       670       680       690       700       710       720
     CAGTGCATACTGTAGGTCATTTTTTTTGCTTCTGGCTACCTGTTTGAAGGGGAGAGAGGGAAAATCAAGTGG
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     CAGTGCATACTGTAGGTCATTTTTTTTGCTTCTGGCTACCTGTTTGAAGGGGAGAGAGGGAAAATCAAGTGG
   650       660       670       680       690       700       710       720

             730       740       750       760       770       780       790
     TATTTTCCAGCACTTTGTATGATTTTGGATGAGCTGTACACCCAAGGATTCTGTTCTGCAACTCCATCCTCC
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     TATTTTCCAGCACTTTGTATGATTTTGGATGAGCTGTACACCCAAGGATTCTGTTCTGCAACTCCATCCTCC
             730       740       750       760       770       780       790

          800       810       820       830       840       850       860
     TGTGTCACTGAATATCAACTCTGAAAGAGCAAACCTAACAGGAGAAAGGACAACCAGGATGAGGATGTCACC
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     TGTGTCACTGAATATCAACTCTGAAAGAGCAAACCTAACAGGAGAAAGGACAACCAGGATGAGGATGTCACC
          800       810       820       830       840       850       860

       870       880       890       900       910       920       930
     AACTGAATTAAACTTAAGTCCAGAAGCCTCCTGTTGGCCTTGGAATATGGCCAAGGCTCTCTCTGTCCCTGT
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     AACTGAATTAAACTTAAGTCCAGAAGCCTCCTGTTGGCCTTGGAATATGGCCAAGGCTCTCTCTGTCCCTGT
       870       880       890       900       910       920       930

     940       950       960       970       980       990      1000
     AAAAGAGAGGGGCAAATAGAGAGTCTCCAAGAGAACGCCCTCATGCTCAGCACATATTTGCATGGGAGGGGG
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     AAAAGAGAGGGGCAAATAGAGAGTCTCCAAGAGAACGCCCTCATGCTCAGCACATATTTGCATGGGAGGGGG
     940       950       960       970       980       990      1000

  1010      1020      1030      1040      1050      1060      1070      1080
     AGATGGGTGGGAGGAGATGAAAATATCAGCTTTTCTTATTCCTTTTTATTCCTTTTAAAATGGTATGCCAAC
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     AGATGGGTGGGAGGAGATGAAAATATCAGCTTTTCTTATTCCTTTTTATTCCTTTTAAAATGGTATGCCAAC
  1010      1020      1030      1040      1050      1060      1070      1080

           1090      1100      1110      1120      1130      1140      1150
     TTAAGTATTTACAGGGTGGCCCAAATAGAACAAGATGCACTCGCTGTGATTTTAAGACAAGCTGTATAAACA
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     TTAAGTATTTACAGGGTGGCCCAAATAGAACAAGATGCACTCGCTGTGATTTTAAGACAAGCTGTATAAACA
           1090      1100      1110      1120      1130      1140      1150

        1160      1170      1180      1190      1200      1210      1220
     GAACTCCACTGCAAGAGGGGGGGCCGGGCCAGGAGAATCTCCGCTTGTCCAAGACAGGGGCCTAAGGAGGGT
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     GAACTCCACTGCAAGAGGGGGGGCCGGGCCAGGAGAATCTCCGCTTGTCCAAGACAGGGGCCTAAGGAGGGT
        1160      1170      1180      1190      1200      1210      1220

      1230      1240      1250      1260      1270      1280      1290
     CTCCACACTGCTGCTAGGGGCTGTTGCATTTTTTTATTAGTAGAAAGTGGAAAGGCCTCTTCTCAACTTTTT
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     CTCCACACTGCTGCTAGGGGCTGTTGCATTTTTTTATTAGTAGAAAGTGGAAAGGCCTCTTCTCAACTTTTT
      1230      1240      1250      1260      1270      1280      1290

    1300      1310      1320      1330      1340      1350      1360
     TCCCTTGGGCTGGAGAATTTAGAATCAGAAGTTTCCTGGAGTTTTCAGGCTATCATATATACTGTATCCTGA
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     TCCCTTGGGCTGGAGAATTTAGAATCAGAAGTTTCCTGGAGTTTTCAGGCTATCATATATACTGTATCCTGA
    1300      1310      1320      1330      1340      1350      1360

  1370      1380      1390      1400      1410      1420      1430      1440
     AAGGCAACATAATTCTTCCTTCCCTCCTTTTAAAATTTGTGTTCCTTTTTGCAGCAATTACTCACTAAAGG
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     AAGGCAACATAATTCTTCCTTCCCTCCTTTTAAAATTTGTGTTCCTTTTTGCAGCAATTACTCACTAAAGG
  1370      1380      1390      1400      1410      1420      1430      1440

           1450      1460      1470      1480      1490      1500      1510
     GCTTCATTTTAGTCCAGATTTTTAGTCTGGCTGCACCTAACTTATGCCTCGCTTATTTAGCCCGAGATCTGG
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
     GCTTCATTTAGTCCAGATTTTTAGTCTGGCTGCACCTAACTTTATGCCTCGCTTATTTAGTCCCGAGATCTGG
     1450                                                          1510
1520 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     TCTTTTTTTTTTTTTTTTTTCCGTCTCCCCAAAAGCTTTATCTGTCTTGACTTTTTTAAAAAAGTTTTGGGG
     1520                                                          1580

     1590                                                          1510
     GCAGATTCTGAATTGGGCTAAAAGAGACATGCATTGTTTTTTAAAATACTTTATTTCTTTATTTTTAAAATAC
1590 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     ATAGCATTAAAATCCCAAAATCCTATTTAAAAGAACTAGCAAC
     1600                                                          1650

1730 TCTGGGTGGTTCTCTGTTGTTAGTCTCTGAGAAATCTTGAGAAATTCTTTGCATTGCAGAGAGGGTAAGAGAGG
     1730                                                          1800
     CTCATGGGTGGGGACATGGAAAAAGAAGGGCAGCCTAGGGCCCTGGGGAGCCCAGTCCACTGAGCAAGCAAGGGAC
     1880                                                          1940

     1950 TGAGTGAGCCTTTTTGCAGGAAAAAGGCTAAGAAAAAAAGGCTAAGAAAAACCATTCTAAAAACAACAAGAAAACTGTCCAA
     1960                                                          2010
```

(DNA sequence alignment blocks 1450–2984; dense sequence data throughout)

SEQ ID NO 335
LENGTH: 2984
TYPE: DNA
ORGANISM: Homo sapien

Initial Score =	Optimized Score = 2984	Significance = 26.07
Residue Identity = 100%	Matches = 2984	Mismatches = 0
Gaps = 0	Conservative Substitutions =	0

A two-column DNA sequence alignment listing spanning residues approximately 1–1650, showing the query sequence (top line of each pair) aligned to an identical reference sequence (bottom line) connected by vertical match bars (|), with numeric position markers (10, 20, 30 … 1650) labeling each segment.

```
1660      1670      1680      1690      1700      1710      1720
ATAGCATTAAATCCTATTTAAAGAAGACCTGACAGCTTCACTACTCGAATTTATAGGACCT
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATAGCATTAAATCCTATTTAAAGAAGACCTGACAGCTTCACTACTCGAATTTATAGGACCT
1660      1670      1680      1690      1700      1710      1720

1730      1740      1750      1760      1770      1780      1790      1800
TCTGGTGGTTCTCTGCTTGTTAGCGTTTGAGTCTGACAATCCTTGAGTATGCAGAGGAGGTAAGAGG
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TCTGGTGGTTCTCTGCTTGTTAGCGTTTGAGTCTGACAATCCTTGAGTATGCAGAGGAGGTAAGAGG
1730      1740      1750      1760      1770      1780      1790      1800

1810      1820      1830      1840      1850      1860      1870
TATTGGATTTCACAGAGGAAGACACAGGCGCCAGGCTTACTGAGCTGTCCAGTGCGAGGG
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TATTGGATTTCACAGAGGAAGACACAGGCGCCAGGCTTACTGAGCTGTCCAGTGCGAGGG
1810      1820      1830      1840      1850      1860      1870

1880      1890      1900      1910      1920      1930      1940
CTCATGGGTGGGAACATGGGAAAAAGGCAGCCTAGGCCCTGGGGGAGGCCCAGTCCACTGAGCAAGGGAC
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CTCATGGGTGGGAACATGGGAAAAAGGCAGCCTAGGCCCTGGGGGAGGCCCAGTCCACTGAGCAAGGGAC
1880      1890      1900      1910      1920      1930      1940

1950      1960      1970      1980      1990      2000      2010
TGAGTGAGCCTTTTGCAGGAAAGGCTAAGAAAAAGGAAAAGGAAAAAACCATTCTAAAACACACAACAGAGAAAACTGTCCAA
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TGAGTGAGCCTTTTGCAGGAAAGGCTAAGAAAAAGGAAAAGGAAAAAACCATTCTAAAACACACAACAGAGAAAACTGTCCAA
1950      1960      1970      1980      1990      2000      2010

2020      2030      2040      2050      2060      2070      2080
ATGCTTTGGGAACTGTGTGTTTATTGCCTATAATGGGTCCCAAAAATGGGGTAACCTAGACTTCAGAGAGAATGA
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATGCTTTGGGAACTGTGTGTTTATTGCCTATAATGGGTCCCAAAAATGGGGTAACCTAGACTTCAGAGAGAATGA
2020      2030      2040      2050      2060      2070      2080

2090      2100      2110      2120      2130      2140      2150      2160
GCAGAGGCAAAGGAGAAAATCTGGCGTCCTTCCATTTTCATTCTGTTATCTCAGGTGAGCTGGTAGAGGGG
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GCAGAGGCAAAGGAGAAAATCTGGCGTCCTTCCATTTTCATTCTGTTATCTCAGGTGAGCTGGTAGAGGGG
2090      2100      2110      2120      2130      2140      2150      2160

2170      2180      2190      2200      2210      2220      2230
AGACATTAGAAAAAAATGAAACAACAACAATTACTAATGAGGTACCGCTGAGGCTGAGGTCTCTTGACT
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AGACATTAGAAAAAAATGAAACAACAACAATTACTAATGAGGTACCGCTGAGGCTGAGGTCTCTTGACT
2170      2180      2190      2200      2210      2220      2230
```

```
2530      2540      2550      2560      2570      2580      2590
TCCCCTCCTCTGAATTTAATTCTTTTCAACTTGCAATTTGCAAGGATTACACATTTCACTGTGATGTATATTG
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TCCCCTCCTCTGAATTTAATTCTTTTCAACTTGCAATTTGCAAGGATTACACATTTCACTGTGATGTATATTG
2530      2540      2550      2560      2570      2580      2590

2600      2610      2620      2630      2640      2650      2660
TGTTGCAAAAAAAAAGTGTCTTTTGTTGTCAAATCCATCTCTTGCTTTTTCCCA
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TGTTGCAAAAAAAAAGTGTCTTTTGTTGTCAAATCCATCTCTTGCTTTTTCCCA
2600      2610      2620      2630      2640      2650      2660

2670      2680      2690      2700      2710      2720      2730
TTGAACTAGTCATTAACCCATCTCTGAACTGGTAGAGAGGCAGCTAGTCTGATCCAGCATCTGAC
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TTGAACTAGTCATTAACCCATCTCTGAACTGGTAGAGAGGCAGCTAGTCTGATCCAGCATCTGAC
2670      2680      2690      2700      2710      2720      2730

2740      2750      2760      2770      2780      2790      2800
AGGTGAATTGGATGGTGTTCTCAGAACCAATTTCACCCAGACCAGCCTGTTTTCTATCCTGTTTAATAAATTAGTTTT
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AGGTGAATTGGATGGTGTTCTCAGAACCAATTTCACCCAGACCAGCCTGTTTTCTATCCTGTTTAATAAATTAGTTTT
2740      2750      2760      2770      2780      2790      2800

2810      2820      2830      2840      2850      2860      2870      2880
CACCCCCACCAAAACTTTATTTTCTATAGTGTTTTTTTGCAACATATGAGTGTTTTTGAAAAATAAAAGTACCCATG
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CACCCCCACCAAAACTTTATTTTCTATAGTGTTTTTTTGCAACATATGAGTGTTTTTGAAAAATAAAAGTACCCATG
2810      2820      2830      2840      2850      2860      2870      2880

2890      2900      2910      2920      2930      2940      2950
GGGTTCTCTACAATCGCATAACAAACCCTCGCTCCAAATCTGTCACATAAAAAGTCTGTTGACTTGAAGTTTAGTCAG
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GGGTTCTCTACAATCGCATAACAAACCCTCGCTCCAAATCTGTCACATAAAAAGTCTGTTGACTTGAAGTTTAGTCAG
2890      2900      2910      2920      2930      2940      2950

2960      2970      2980
TCTTTATTAGAAAAAAAAAAAAAAAA
||||||||||||||||||||||||||
TCTTTATTAGAAAAAAAAAAAAAAAA
2960      2970      2980
```

```
10        20        30        40        50        60        70
ATCCCTCCTTCCCCACTCTCCTTTCCAGAGAGGCACTTGGGGTCTTATCCTGTGTTGGGACTCTGAAAAACACTTCAG
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCCCTCCTTCCCCACTCTCCTTTCCAGAGAGGCACTTGGGGTCTTATCCTGTGTTGGGACTCTGAAAAACACTTCAG
10        20        30        40        50        60        70
```

```
|||||||||||||||||||||||||||||||||||||||||||||||||||
TATTGGAATTTCACAGAGAGAACACACGCAGAAATGAAGAGGGGCCAGGGCTTACTGAGCTGTGTCCAGTGGAGGG
1810    1820    1830    1840    1850    1860    1870

1880
CTCATGGGTGGGACATGGAAAGAAAAGGCAGCCTAGGGCCTGGGGGAGGCCAGTCCACTGAGCAAGCAAGGGAC
1880    1890    1900    1910    1920    1930    1940

1950
TCAGTGAGCCTTTTGCAGGAAAAGGGCTTAAGAAAAGGAAAAAACCATTCTAAAACACAACAAGAAACTGTCCAA
1950    1960    1970    1980    1990    2000    2010

2020
ATGCTTTGGGAACTGTGTGTTTAATTGCCTATAATGGGTCCCAAAAATGGGTAACCTAGAACTTCAGAGAATGA
2020    2030    2040    2050    2060    2070    2080

2090
GCAGAGAGCAAAGGAGAAAATCTGGGCTGTGTCCTTCCATTTTCATTCTGTTATCTCAGGTGAGCTGTAGAGGGG
2090    2100    2110    2120    2130    2140    2150    2160

2170
AGACATTAGAAAAAAATGAAACAACAAAAACAATTACTAATGAGGTACCGTGGGAGGTTCTTCTTGACT
2170    2180    2190    2200    2210    2220    2230

2240
CCACTACTTAATTCCGTTTAGTGAGAAAACCTTTCAATTTTCTTTTATTGAAGGGGCCAGCTTACTGTTGGTG
2240    2250    2260    2270    2280    2290    2300

2310
GCAAAAATTGCCAACATAAGTTAATAGAAAAGTTCGGCCAAATTTCACCCCATTTTCGTGGTTTGGGCTCCACAT
2310    2320    2330    2340    2350    2360    2370

2380
TGCAAAGTTCAATGCCACGTGCTGCTGACCGACCGGAGTACTGACCCAGCACAAAAGGCAGGGTAGCCTGA
2380    2390    2400    2410    2420    2430    2440

2450
ATTGCTTTCTGCTCTTTACATTTCTTTTAAAATAAGCATTTAGTGCTGAGTCCCTACTGAGTACTCTTTCTC
2450    2460    2470    2480    2490    2500    2510    2520

2530
TCCCCTCCTCTGAATTTAATTCTTTCAAGGATTACACATTTCACTGTGTGATTGTATATTG
2530    2540    2550    2560    2570    2580    2590

2600
TGTTGCAAAAAAAAAAAAAGTGTCTTTTGTTTGTGAATCCATCCTTGCTTTTCCCCA
2600    2610    2620    2630    2640    2650    2660

2670
TTGGAACTAGTCATTAACCCATCTCTGAACTGGTAGAAAAACATCTGACAGAGCTAGTCTATCAGCATCTGAC
2670    2680    2690    2700    2710    2720    2730
```

4. US-09-439-313-335 (1-2984)
US-09-352-616A-4 Sequence 434, Application US/09352616A

Sequence 434, Application US/09352616A
Patent No. 6395278
GENERAL INFORMATION:
  APPLICANT: Dillon, Davin C.
  APPLICANT: Harlocker, Susan Louise
  APPLICANT: Jiang, Yuqui
  APPLICANT: Xu, Jiangchun
  APPLICANT: Mitcham, Jennifer Lynn
  TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
  TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
  FILE REFERENCE: 210121.427C8
  CURRENT APPLICATION NUMBER: US/09/352,616A
  CURRENT FILING DATE: 1999-07-13
  NUMBER OF SEQ ID NOS: 472
  SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 434
  LENGTH: 484
  TYPE: DNA
  ORGANISM: Homo sapiens

Initial Score   = 358   Optimized Score = 483   Significance = 2.77
Residue Identity   = 99%   Matches   = 484   Mismatches   = 0
Gaps   = 2   Conservative Substitutions = 0

```
TTGGAACTAGTCATTAACCCATCTCTGAACTGGTAGAAAAACATCTGACAGAGCTAGTCTATCAGCATCTGAC
2670    2680    2690    2700    2710    2720    2730

2740
AGGTGAAATTGGATGGTGTTCTCAGAACCATTTCACCCAGACAGCCCTGTTTGTTTCTATCCTGTTTAATAAATTAGTTT
2740    2750    2760    2770    2780    2790    2800

2810
GGGTTCTCTACATGCATAACAAACCCTTGTCCAATCTGTCACATAATGAGGTGTTGTGATCCTGTGACTTGAAGTTTAGTCAG
2810    2820    2830    2840    2850    2860    2870    2880

2890
CACCCCACCAAAACTTTATTTTATTTCTATGGTGTTTTTTGCAACACATAATGAGGTGTTTTGAAAATAAAGTACCCATG
2890    2900    2910    2920    2930    2940    2950

2960
TCTTTATTAGAAAAAAAAAAAAAAAAAAAAAA
2960    2970    2980    X

2430
CCAGCACAAAAGGCAGGGTAGCCTGAAATGCTTTCTGCTCTTTACATTTCTTTTAAAATAAGCATTTAGTGC
2430    2440    2450    2460    2470    2480    2490

2500
TCAGTCCCTACTGAGTACTCTTTCTCTCCCCTCCTCTGAATTTAATTCTTTCAACTTGCAAGGAT
2500    2510    2520    2530    2540    2550    2560

2570
TACACATTTCACTGTGATGTATATTGTGTTGCAAAAAAAAAAAAAAAGTGTCTTTTGTTTGTTTACTTGGTT
2570    2580    2590    2600    2610    2620    2630

100
TACACATTTCAACTGTGATGTATAATGTGTGTTGC--AAAAAAAAAAAAAAAAATTACTTGGTT
100    110    120    130    140    150    160
```

5. US-09-439-313-335 (1-2984)
   US-09-352-616A-4 Sequence 453, Application US/0935616A

```
                2640      2650      2660      2670      2680      2690      2700      2710
TGTGAATCCATCTTGCTTTTTCCCCATTGGAAACTAGTCAGTTCAGTAAGCTGGTAGAAAAACAATCT
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TGTTGAATCCATCCTTGCTTTTTCCCCATTGGAAACTAGTCAGTTCAGTAAGCTGGTAGAAAAACAATCT
  170       180       190       200       210       220       230

                2720      2730      2740      2750      2760      2770      2780
GAAGAGCTAGTTCATCTGACCAGGTGAAATTGGATGGTTCTTCAGAACCATTTCACCCAGACAGCCTGT
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GAAGAGCTAGTTCATCTGACCAGGTGAAATTGGATGGTTCTTCAGAACCATTTCACCCAGACAGCCTGT
  240       250       260       270       280       290       300

                2790      2800      2810      2820      2830      2840      2850
TTCTATCCTGTTTAATAAATTAGTTTGGGTTCTCTACATGCATAACAAACCCTGCTCCAAATCTGTCACATAA
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TTCTATCCTGTTTAATAAATTAGTTTGGGTTCTCTACATGCATAACAAACCCTGCTCCAAATCTGTCACATAA
  310       320       330       340       350       360       370       380

                2860      2870      2880      2890      2900      2910      2920
AAGTCTGTGACTTGAAGTTTAGTCAGCACCCCCACCACAAACTTTATTTTTCTATGTGTTTTTTGCAACATATG
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AAGTCTGTGACTTGAAGTTTAGTCAGCACCCCCACCACAAACTTTATTTTTCTATGTGTTTTTTGCAACATATG
  390       400       410       420       430       440       450

                2930      2940      2950      2960      2970      2980
AGTGTTTTGAAAAATAAAGTACCCATGTCTTTA
||||||||||||||||||||||||
AGTGTTTTGAAAAATAAAGTACCCATGTCTTTA
  460       470       480      X
```

Sequence 453, Application US/0935616A
Patent No. 6395278
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqui
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 453
LENGTH: 317
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(317)
OTHER INFORMATION: n = A,T,C or G

```
Initial Score    = 310   Optimized Score         = 311   Significance = 2.34
Residue Identity = 98%   Matches                 = 311   Mismatches   = 6
Gaps             = 0     Conservative Substitutions = 0
```

```
                2600      2610      2620      2630      2640      2650      2660
TTGCAAAAAAAAAAAAAGTGTTCTTTGTTGAAATTACTTGGTTGTGAAATCCATCTTGCTTTTTTCCCCATT
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                                     TACATCTTGCTTTTTTCCCCATT
                                                      X         10        20

                2670      2680      2690      2700      2710      2720      2730
GGAACTAGTCATTAACCATCTCTGAACTGGGTAGAAAAACATCTGAAGAGCTAGTTCATCTGACCATCTGACCAG
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GGAACTAGTCATTAACCATCTCTGAACTGGGTAGAAAAACATCTGAAGAGCTAGTTCATCAGCATCTGGCAA
  30        40        50        60        70        80        90
```

6. US-09-439-313-335 (1-2984)
   US-09-020-956-11 Sequence 115, Application US/09020956

```
                2740      2750      2760      2770      2780      2790      2800      2810
GTGAATTGGATGGTTCTTCAGAACCATTTCACCCAGACAGCAGCCTGTTTCTATCCTGTTTAATAAATTAGTTTGG
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GTGAATTGGATGGTTCTTCAGAACCATTTCACCCAGACAGCAGCCTGTTTCTATCCTGTTTAATAAATTAGTTTGG
  100       110       120       130       140       150       160

                2820      2830      2840      2850      2860      2870      2880
GTTCTCTACATGCATAACAAACCCTGCTCCAAATCTGTCACATAAAAAGTCTGTGACTTGAAGTTTAGTCAGCA
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GTTCTCTACATGCATAACAAACCCTGCTCCAAATCTGTCACATAAAAAGTCTGTGACTTGAAGTTTAGTCAGCA
  170       180       190       200       210       220       230

                2890      2900      2910      2920      2930      2940      2950
CCCCCACCACAAACTTTATTTTTCTATGTGTTTTTTGCAACATATGAGTGTTTTGAAAAATAAAGTACCCATGTC
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CCCCCACCACAAACTTTATTTTTCTATGTGTTTTTTGCAACATATGAGTGTTTTGAAAAATAAAGTACCCATGTC
  240       250       260       270       280       290       300       310

                2960      2970      2980
TTTATTA
|||||||
TTTATTA
  X
```

Sequence 115, Application US/09020956
Patent No. 6261562
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillin, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,956
FILING DATE: 09-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C2
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 115
SEQUENCE CHARACTERISTICS:
LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo Sapiens

```
Initial Score    = 278   Optimized Score         = 364   Significance = 2.06
Residue Identity = 99%   Matches                 = 365   Mismatches   = 1
Gaps             = 2     Conservative Substitutions = 0
```

Left column

```
        2470       2480       2490       2500       2510       2520       2530
TCTTTACATTTCTTTTAAAATAAGCATTTAGTGCTCAGTCCCTACTGAGTACTCTTTCTCTCCCCTCCTCTG
                                                    ||||||||||||||||||||||
                                                    GCTCTTTCTCTCCCCTCCTCTG
                                                    X         10        20

        2540       2550       2560       2570       2580       2590       2600
AAATTTAATTCTTTCAACTTGCAATTTGCAAGGAATTACACATTTCACTCTGTGATGTATATGTTGTGCAAAAAA
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||
AAATTTAATTCTTTCAACTTGCAATTTGCAAGGAATTACACATTTCACTCTGTGATGTATATGTTGTGC--AAAA
        30         40         50         60         70         80         90

        2610       2620       2630       2640       2650       2660       2670
AAAAAAAGTGTCTTTTGTTTAAAATTACTTGGTTTGTTGTGAAATCCATTCCCCATTGGAACTAGTC
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AAAAAAGTGTCTTTTGTTTAAAATTACTTGGTTTGTTGTGAAATCCATTCCCCATTGGAACTAGTC
       100        110        120        130        140        150        160

        2680       2690       2700       2710       2720       2730       2740
TGCATAACAAAACCCTGCTCCAATCTGTCACATAAAAAGTCTGTGACTTGGAAGTTTAGTCAGCACCCCACCAA
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATTAACCCATCTCTGAACTGGTAGAGAGCTAGTCTCATCAGCATCACAGGTGAATTGGA
       170        180        190        200        210        220        230

        2750       2760       2770       2780       2790       2800       2810
TGGTTCTCAGAACCATTTCACCCCAGACAGCCTGTTCTTTCTATCCTGTTTAATAAATTAGTTTGGGTTTCTCTACA
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATTAACCCATCTCTGAACTGGTAGAGAGCTAGTCTCATCAGCATCACAGGTGAATTGGA
       240        250        260        270        280        290        300

        2830       2840       2850       2860       2870       2880       2890
TGCATAACAAAACCCTGCTCCAATCTGTCACATAAAAAGTCTGTGACTTGGAAGTTTAGTCAGCACCCCACCAA
       310        320        330        340        350        360

        2900       2910       2920
ACTTTATTTTCTATGTGTTTTTTGCAACATATGAG
```

7. US-09-439-313-335 (1-2984)
US-09-030-607-11 Sequence 115, Application US/09030607

Sequence 115, Application US/09030607
Patent No. 6262245
GENERAL INFORMATION:
   APPLICANT: Xu, Jiangchun
   APPLICANT: Dillon, Davin C.
   TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
   NUMBER OF SEQUENCES: 224
   CORRESPONDENCE ADDRESS:
      ADDRESSEE: SEED and BERRY LLP
      STREET: 6300 Columbia Center, 701 Fifth Avenue
      CITY: Seattle
      STATE: WA
      COUNTRY: USA
      ZIP: 98104
   COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patentin Release #1.0, Version #1.30
   CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/09/030,607
      FILING DATE: 25-FEB-1998
      CLASSIFICATION:
   ATTORNEY/AGENT INFORMATION:
      NAME: Maki, David J.
      REGISTRATION NUMBER: 31,392
      REFERENCE/DOCKET NUMBER: 210121.427C3
   TELECOMMUNICATION INFORMATION:
      TELEPHONE: (206) 622-4900
      TELEFAX: (206) 682-6031

Right column

INFORMATION FOR SEQ ID NO: 115:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 366 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: cDNA
  ORIGINAL SOURCE:
    ORGANISM: Homo sapiens

```
Initial Score     = 278   Optimized Score = 364   Significance = 2.06
Residue Identity  = 99%   Matches         = 365   Mismatches   = 1
Gaps              = 2     Conservative Substitutions      = 0
```

```
        2470       2480       2490       2500       2510       2520       2530
TCTTTACATTTCTTTTAAAATAAGCATTTAGTGCTCAGTCCCTACTGAGTACTCTTTCTCTCCCCTCCTCTG
                                                    ||||||||||||||||||||||
                                                    GCTCTTTCTCTCCCCTCCTCTG
                                                    X         10        20

        2540       2550       2560       2570       2580       2590       2600
AAATTTAATTCTTTCAACTTGCAATTTGCAAGGAATTACACATTTCACTCTGTGATGTATATGTTGTGCAAAAAA
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||
AAATTTAATTCTTTCAACTTGCAATTTGCAAGGAATTACACATTTCACTCTGTGATGTATATGTTGTGC--AAAA
        30         40         50         60         70         80         90

        2610       2620       2630       2640       2650       2660       2670
AAAAAAAGTGTCTTTTGTTTAAAATTACTTGGTTTGTTGTGAAATCCATTCCCCATTGGAACTAGTC
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AAAAAAGTGTCTTTTGTTTAAAATTACTTGGTTTGTTGTGAAATCCATTCCCCATTGGAACTAGTC
       100        110        120        130        140        150        160

        2680       2690       2700       2710       2720       2730       2740
ATTAACCCATCTCTGAACTGGTAGAGAGCTAGTCTCATCAGCATCACAGGTGAATTGGA
       170        180        190        200        210        220        230

        2750       2760       2770       2780       2790       2800       2810
TGGTTCTCAGAACCATTTCACCCCAGACAGCCTGTTCTTTCTATCCTGTTTAATAAATTAGTTTGGGTTTCTCTACA
       240        250        260        270        280        290        300

        2830       2840       2850       2860       2870       2880       2890
TGCATAACAAAACCCTGCTCCAATCTGTCACATAAAAAGTCTGTGACTTGGAAGTTTAGTCAGCACCCCACCAA
       310        320        330        340        350        360

        2900       2910       2920
ACTTTATTTTCTATGTGTTTTTTGCAACATATGAG
```

8. US-09-439-313-335 (1-2984)
US-09-352-616A-1 Sequence 115, Application US/09352616A

Sequence 115, Application US/09352616A
Patent No. 6395278
GENERAL INFORMATION:
   APPLICANT: Dillon, Davin C.
   APPLICANT: Harlocker, Susan Louise
   APPLICANT: Jiang, Yuqui
   APPLICANT: Xu, Jiangchun
   APPLICANT: Mitcham, Jennifer Lynn
   TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
   TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
   FILE REFERENCE: 210121.427C8
   CURRENT APPLICATION NUMBER: US/09/352,616A
   CURRENT FILING DATE: 1999-07-13
   NUMBER OF SEQ ID NOS: 472
   SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 115

Left column

LENGTH: 366
TYPE: DNA
ORGANISM: Homo sapien

Initial Score =	278	Optimized Score =	364	Significance =	2.06
Residue Identity =	99%	Matches =	365	Mismatches =	1
Gaps =	2	Conservative Substitutions =	0		

```
        2470       2480       2490       2500       2510       2520       2530
TCTTTACATTTCTTTTAAAATAAGCATTTAGTGCTCAGTCCCTACTGAGTACTCTTTTCTCTCCCCTCCCCTCTG
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                                   GCTCTTTCTCTCCCCTCCCCTCTG
                                                   X         10         20
```

```
        2540       2550       2560       2570       2580       2590       2600
AATTTAATTCTTTCAACTTGCAAGGATTACACATTTCACTGTGATGTGATGTATATGTGTGTTGTTGCAAAAAAA
                                                                    GC--AAAA
        30         40         50         60         70         80         90
```

```
        2610       2620       2630       2640       2650       2660       2670
AAAAAAAGTGTCTTTTGTTTTGTTTAAAAATTACTTGGTTTGTGAAATCCATCCATCCTTGCTTTTCCCATTGGAACTAGTC
        100        110        120        130        140        150        160
```

```
        2680       2690       2700       2710       2720       2730       2740
ATTAACCCATCTCTGAACTGGTAGAAAAAACATTCTGAAGAGGCTAGTCTATCAGCAGCATCTGACAGGTGAAATTGGA
        170        180        190        200        210        220        230
```

```
        2750       2760       2770       2780       2790       2800       2810       2820
TGGGTTCTCAGAACCAATTCACCCAGACAGCCCTGTTTCTATCCTGTTGTTTTAATATTAGTTGGGTTCTCTACA
        240        250        260        270        280        290        300
```

```
        2830       2840       2850       2860       2870       2880       2890
TGCATAACAAAACCCTGCTCCAAATCGTCACATAAAAAGTCTGTGACTTGAAGTTTACTTCAGCACCCCACCAA
        310        320        330        340        350        360
```

```
        2900       2910       2920
ACTTTAATTTTCTATGTGTGTTTTTGCAACATATGAG
```

9. US-09-439-313-335 (1-2984)
   US-09-232-149A-1 Sequence 115, Application US/09232149A

Sequence 115, Application US/09232149A
Patent No. 6465611
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
   CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.42706
CURRENT APPLICATION NUMBER: US/09/232,149A
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 115
LENGTH: 366
TYPE: DNA
ORGANISM: Homo sapien

Right column

10. US-09-439-313-335 (1-2984)
    US-09-159-812-11 Sequence 115, Application US/09159812A

Sequence 115, Application US/09159812A
Patent No. 6613872
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.428C5
CURRENT APPLICATION NUMBER: US/09/159,812A
CURRENT FILING DATE: 1998-09-23
NUMBER OF SEQ ID NOS: 306
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 115
LENGTH: 366
TYPE: DNA
ORGANISM: Homo sapien

Initial Score =	278	Optimized Score =	364	Significance =	2.06
Residue Identity =	99%	Matches =	365	Mismatches =	1
Gaps =	2	Conservative Substitutions =	0		

```
        2470       2480       2490       2500       2510       2520       2530
TCTTTACATTTCTTTTAAAATAAGCATTTAGTGCTCAGTCCCTACTGAGTACTCTTTTCTCTCCCCTCCCCTCTG
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                                   GCTCTTTCTCTCCCCTCCCCTCTG
                                                   X         10         20
```

```
        2540       2550       2560       2570       2580       2590       2600
AATTTAATTCTTTCAACTTGCAAGGATTACACATTTCACTGTGATGTGATGTATATGTGTGTTGTTGCAAAAAAA
                                                                    GC--AAAA
```

Left column

```
11. US-09-439-313-335 (1-2984)
    US-09-115-453-11 Sequence 115, Application US/0911545B

GENERAL INFORMATION:
    Sequence 115, Application US/0911545B
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
TITLE OF INVENTION: METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C4
CURRENT APPLICATION NUMBER: US/09/115,453B
CURRENT FILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 115
LENGTH: 366
TYPE: DNA
ORGANISM: Homo sapien

Initial Score   =  278   Optimized Score =  364   Significance = 2.06
Residue Identity =  99%   Matches         =  365   Mismatches   =  1
Gaps             =  2     Conservative Substitutions = 0
```

Right column

```
12. US-09-439-313-335 (1-2984)
    US-09-288-946-11 Sequence 115, Application US/09288946

GENERAL INFORMATION:
    Sequence 115, Application US/09288946
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C7
CURRENT APPLICATION NUMBER: US/09/288,946
CURRENT FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 381
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 115
LENGTH: 366
TYPE: DNA
ORGANISM: Homo sapien

Initial Score   =  278   Optimized Score =  364   Significance = 2.06
Residue Identity =  99%   Matches         =  365   Mismatches   =  1
Gaps             =  2     Conservative Substitutions = 0
```

(Page also contains dense DNA sequence alignment blocks with residue position markers from 30 through 360 and corresponding base-pair position numbers from 2470 through 2900+.)

Left portion

```
         240       250       260       270       280       290       300
      2830      2840      2850      2860      2870      2880      2890
TGCATAACAAAACCCTGCTCCAATCTGTCACATAAAAAGTCTGTTGAGTTTAGTCAGCAGACCCCCACCAA
TGCATAACAAAACCCTGCTCCAATCTGTCACATAAAAAGTCTGTTGAGTTTAGTCAGCAGACCCCCACCAA
310       320       330       340       350       360      X

      2900      2910      2920
ACTTTATTTTCTATGTGTTTTTTTGCAACATATGAG
```

13. US-09-439-313-335 (1-2984)
    US-09-030-607-20 Sequence 207, Application US/09030607

Sequence 207, Application US/09030607
Patent No. 6262245
GENERAL INFORMATION:
  APPLICANT: Xu, Jiangchun
  APPLICANT: Dillon, Davin C.
  TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
  NUMBER OF SEQUENCES: 224
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: SEED and BERRY LLP
    STREET: 6300 Columbia Center, 701 Fifth Avenue
    CITY: Seattle
    STATE: WA
    COUNTRY: USA
    ZIP: 98104
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/030,607
    FILING DATE: 25-FEB-1998
    CLASSIFICATION:
  ATTORNEY/AGENT INFORMATION:
    NAME: Maki, David J.
    REGISTRATION NUMBER: 31,392
    REFERENCE/DOCKET NUMBER: 210121.427C3
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (206) 622-4900
    TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 207:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 332 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
    MOLECULE TYPE: cDNA

```
Initial Score       =    253    Optimized Score  =   318    Significance  =  1.84
Residue Identity    =    96%    Matches          =   322    Mismatches    =  7
Gaps                =    4      Conservative Substitutions =  0

      1550      1560      1570      1580      1590  X   1600      1610
CCCAAAGCTTTATCTGTCTTGACTTTTTAAAAAAGTTTGGGGGGCAGATTCTGAATTGGCTAAAAGACATGCA
                                                  |||||||||||||||||||  ||||
                                                TGAATTGGCTAAAAGAC-TGCA
                                                         X        10       20

      1620      1630      1640      1650      1660      1670      1680
TTTTTAAAACTAGCAACTCTTATTTTTCTTTAAAAAAATACATAGCATTAAAATCCAAAATCCTATTTAAAG
TTTTTANAACTAGCAACTCTTATTTTTCTTTAAAAAATACATAGCATTAAAATCCAAAATCCTATTTAAAG
         30        40        50        60        70        80        90

      1690      1700      1710      1720      1730      1740      1750
ACCTGACAGCTTGAGAGAGGTCACTACTGCATTTATAGGACCTTCTCTGGTGGTTCTCGCTGTTTACGTTTGAAGTC
ACCTGACAGCTTGAGAGAGGTCACTACTGCATTTATAGGACCTTCTCTGGTGGTTCTCGCTGTTTACNTTTGAAGTC
        100       110       120       130       140       150       160
```

Right portion

14. US-09-439-313-335 (1-2984)
    US-09-352-616A-2 Sequence 207, Application US/09352616A

Sequence 207, Application US/09352616A
Patent No. 6395278
GENERAL INFORMATION:
  APPLICANT: Dillon, Davin C.
  APPLICANT: Harlocker, Susan Louise
  APPLICANT: Jiang, Yuqui
  APPLICANT: Xu, Jiangchun
  APPLICANT: Mitcham, Jennifer Lynn
  TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
  TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
  FILE REFERENCE: 210121.427C8
  CURRENT APPLICATION NUMBER: US/09/352,616A
  CURRENT FILING DATE: 1999-07-13
  NUMBER OF SEQ ID NOS: 472
  SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 207
  LENGTH: 332
  TYPE: DNA
  ORGANISM: Homo sapien
  FEATURE:
  NAME/KEY: misc_feature
  LOCATION: (1)..(332)
  OTHER INFORMATION: n = A,T,C or G

A

```
         100       110       120       130       140       150       160
      1760      1770      1780      1790      1800      1810      1820      1830
TGACAAATCCTTGCAAATCTTTGCATGCAGAGAGAGGTAAGAGGTATTGGGATTTTCACAGAGAGGAAGAACACAGC
TGACAAATCCTTGNAAATCTTTGCATGCAGAGAGAGGTAAGAGGTATTGGGATTTTCACAGAGAGGAAGAACACAGC
         170       180       190       200       210       220       230

      1840      1850      1860      1870      1880      1890
GCAG-AATGAA-GGGCCAGGCTTACTGAGC-TGTCCAGTGGGAGGGGCTCAATGGGTGGGGGGACATGGAAAAAGAAGG
||||||||||||  ||||  |||||||||||  ||||||||||||||||||||||||  |||||||  |||||||||||
GCAGAAATGAAGGGGCCCAGGCTTACTGAGCTTGTCCAGTGGGAGGGGCTCAATGGGTGGGGGGACATGGAAAAAGAAGG
         240       250       260       270       280       290       300

      1900      1910      1920  X   1930      1940      1950      1960      1970
CAGCCCTAGGCCCTGGGGGAGCCCAGTCCACTGAGCAAGCAAGGGACCCTTTTGCAGGAAAAAGGCT
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CAGCCCTAGGCCCTGGGGGAGCCCA
         310       320       330  X
```

```
Initial Score       =    253    Optimized Score  =   318    Significance  =  1.84
Residue Identity    =    96%    Matches          =   322    Mismatches    =  7
Gaps                =    4      Conservative Substitutions =  0

      1550      1560      1570      1580      1590  X   1600      1610
CCCAAAGCTTTATCTGTCTTGACTTTTTAAAAAAGTTTGGGGGGCAGATTCTGAATTGGCTAAAAGACATGCA
                                                  |||||||||||||||||||  ||||
                                                TGAATTGGCTAAAAGAC-TGCA
                                                         X        10       20

      1620      1630      1640      1650      1660      1670      1680
TTTTTAAAACTAGCAACTCTTATTTTTCTTTAAAAAAATACATAGCATTAAAATCCAAAATCCTATTTAAAG
TTTTTANAACTAGCAACTCTTATTTTTCTTTAAAAAATACATAGCATTAAAATCCAAAATCCTATTTAAAG
         30        40        50        60        70        80        90

      1690      1700      1710      1720      1730      1740      1750
ACCTGACAGCTTGAGAGAGGTCACTACTGCATTTATAGGACCTTCTCTGGTGGTTCTCGCTGTTTACGTTTGAAGTC
ACCTGACAGCTTGAGAGAGGTCACTACTGCATTTATAGGACCTTCTCTGGTGGTTCTCGCTGTTTACNTTTGAANTC
        100       110       120       130       140       150       160
```

Left column

```
        1760        1770        1780        1790        1800        1810        1820        1830
   TGACAATCCTTGANAATCTTTGCATGCAGAGGAGGAGGTAATTGGATTTTTCACAGAGGAGGAGGAAGAACAGC
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   TGACAATCCTTGANAATCTTTGCATGCAGAGGAGGAGGTAATTGGATTTTTCACAGAGGAGGAGGAAGAACAGC
        170         180
```

```
        1690        1700        1710        1720        1730        1740        1750
   ACCTGACAGCTTGAGAAGGTCACTACTGCCATTTATAGGACCTTCTGGTGGTTGTTACGTTGTTACTTTTGAAGTC
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   ACCTGACAGCTTGAGAAGGTCACTACTGCCATTTATAGGACCTTCTGGTGGTTGTTCTGCTGTTACNTTTGAANTC
        100         110         120         130         140         150         160
```

```
        1620        1630        1640        1650        1660        1670        1680
   TTTTTANAACTAGCAACTCTTATTTCTTTCCTTTAAAAAATACATAGCATTAAAATCCCAAAATCCTATTTAAAG
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   TTTTTANAACTAGCAACTCTTATTTCTTTCCTTTAAAAAATACATAGCATTAAAATCCCAAAATCCTATTTAAAG
        30          40          50          60          70          80          90
```

```
        1550        1560        1570        1580        1590        1600        1610
   CCCAAAGCTTTATCTGTCTTGACTTTTTTAAAAAAGTTTGGGGGGGCAGAATTCTGAATTGGCTAAAAGACATGCA
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
                                                             TGAATTGGCTAAAAGAC-TGCA
                                                             X  1600  X  1610
```

```
Initial Score       =   253    Optimized Score   =   318    Significance  =  1.84
Residue Identity    =   96%    Matches           =   322    Mismatches    =  7
Gaps                =   4      Conservative Substitutions  X          10        20
                                                           =   0
```

16. US-09-439-313-335 (1-2984)
    US-09-232-149A-2 Sequence 207, Application US/0923214A

```
A
```

```
        1900        1910        1920 X      1930        1940        1950        1960        1970
   CAGCCTAGGCCCTGGGGAGGGACCCCCCCCCCCCTGAGGAGCAAGCAGGGACTGAGTGAGCCCTTTTGCAGGAAAAAGGCT
   |||||||||||||||||||||
   CAGCCTAGGCCCTGGGGAGGCCCA
        310         320         330 X
```

```
        1840        1850        1860        1870        1880        1890
   GCAG-AATGAA-GGGCCAGGCTTACTGAGC-TGTCCAGTGGAGGGCTCATGGGGTTGGGGGGACATGGGGAAAAAAGAAGG
   ||||  |||||||  ||||||||||  |||| |||||||||||||||| |||||||| ||||||||| |||||||||||||||
   GCAGAAATGAAGGGGCCAGGCTTACTGAGCTTGTTCCACTGGAGGGGCTCATGGGGTTGGGGGGACATGGGGAAAAAAGGCT
        240         250         260         270         280         290         300
```

```
        170         180
   TGACAATCCTTGANAATCTTTGCAT...
```

```
SEQ ID NO 207
LENGTH: 332
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(332)
OTHER INFORMATION: n = A,T,C or G
```

```
Sequence 207, Application US/0923214A
Patent No. 6446561
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C6
CURRENT APPLICATION NUMBER: US/09/232,149A
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FastSEQ for Windows Version 3.0
```

15. US-09-439-313-335 (1-2984)
    US-09-232-149A-2 Sequence 207, Application US/0923214A

Right column

```
        1840        1850        1860        1870        1880        1890
   GCAG-AATGAA-GGGCCAGGCTTACTGAGC-TGTCCAGTGGAGGGCTCATGGGGTTGGGGGGACATGGGGAAAAAAGAAGG
   ||||  |||||||  ||||||||||  |||| |||||||||||||||| |||||||| ||||||||| |||||||||||||||
   GCAGAAATGAAGGGGCCAGGCTTACTGAGCTTGTTCCACTGGAGGGGCTCATGGGGTTGGGGGGACATGGGGAAAAAAGGCT
        240         250         260         270         280         290         300
```

```
        1900        1910        1920 X      1930        1940        1950        1960        1970
   CAGCCTAGGCCCTGGGGAGGGACCCCCCCCCCCCTGAGGAGCAAGCAGGGACTGAGTGAGCCCTTTTGCAGGAAAAAGGCT
   |||||||||||||||||||||
   CAGCCTAGGCCCTGGGGAGGCCCA
        310         320         330 X
```

```
A
```

```
SEQ ID NO 207
LENGTH: 332
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(332)
OTHER INFORMATION: n = A,T,C or G
```

```
Sequence 207, Application US/09159812A
Patent No. 6613872
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.428C5
CURRENT APPLICATION NUMBER: US/09/159,812A
CURRENT FILING DATE: 1998-09-23
NUMBER OF SEQ ID NOS: 306
SOFTWARE: FastSEQ for Windows Version 3.0
```

16. US-09-439-313-335 (1-2984)
    US-09-159-812-20 Sequence 207, Application US/09159812A

```
Initial Score       =   253    Optimized Score   =   318    Significance  =  1.84
Residue Identity    =   96%    Matches           =   322    Mismatches    =  7
Gaps                =   4      Conservative Substitutions  X          10        20
                                                           =   0
```

```
        1550        1560        1570        1580        1590        1600        1610
   CCCAAAGCTTTATCTGTCTTGACTTTTTTAAAAAAGTTTGGGGGGGCAGAATTCTGAATTGGCTAAAAGACATGCA
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
                                                             TGAATTGGCTAAAAGAC-TGCA
                                                             X           10        20
```

```
        1620        1630        1640        1650        1660        1670        1680
   TTTTTANAACTAGCAACTCTTATTTCTTTCCTTTAAAAAATACATAGCATTAAAATCCCAAAATCCTATTTAAAG
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   TTTTTANAACTAGCAACTCTTATTTCTTTCCTTTAAAAAATACATAGCATTAAAATCCCAAAATCCTATTTAAAG
        30          40          50          60          70          80          90
```

```
        1690        1700        1710        1720        1730        1740        1750
   ACCTGACAGCTTGAGAAGGTCACTACTGCCATTTATAGGACCTTCTGGTGGTTGTTCTGCTGTTACNTTTGAANTC
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   ACCTGACAGCTTGAGAAGGTCACTACTGCCATTTATAGGACCTTCTGGTGGTTGTTCTGCTGTTACNTTTGAANTC
        100         110         120         130         140         150         160
```

```
        1760        1770        1780        1790        1800        1810        1820        1830
   TGACAATCCTTGANAATCTTTGCATGCAGAGGAGGAGGTAATTGGATTTTTCACAGAGGAGGAGGAANAACAGC
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   TGACAATCCTTGANAATCTTTGCATGCAGAGGAGGAGGTAATTGGATTTTTCACAGAGGAGGAGGAANAACAGC
        170         180         190         200         210         220         230
```

```
        1840        1850        1860        1870        1880        1890
   GCAG-AATGAA-GGGCCAGGCTTACTGAGC-TGTCCAGTGGAGGGCTCATGTGGGTTGGGGGACATGGGGAAAAAAGAAGG
   ||||  ||||||  |||||
   GCAG-AATGAA -GGGCCA...
        170         180         190         200         210         220         230
```

Left column:

```
             240    250      260      270      280      290      300
GCAGAAAATGAAGGGGCCCAGGCTTACTGAGCTTGTCCACTGGATGGGGTGGGACATGGAAAAAGAAGG
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CAGCCTAGGCCCCTGGGGAGGAGCCCAGTCCACTGAGCAAGCAAGGGACTGAGTGAGCCTTTTGCAGGAAAAGGCT
          310    320      330 X

     1900    1910    1920 X   1930    1940    1950    1960    1970
CAGCCTAGGCCCCTGGGGAGGAGCCCA
||||||||||||||||||||||||||
CAGCCTAGGCCCTGGGGAGCCCA
          310    320    330 X
```

A

---

17. US-09-439-313-335 (1-2984)
   US-09-115-453-20 Sequence 207, Application US/09115453B

   A

Sequence 207, Application US/09115453B
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
TITLE OF INVENTION: METHODS FOR THEIR USE
FILE REFERENCE: 210121.42704
CURRENT APPLICATION NUMBER: US/09/115,453B
CURRENT FILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 207
LENGTH: 332
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(332)
OTHER INFORMATION: n = A,T,C or G

Initial Score = 253	Optimized Score = 318	Significance = 1.84
Residue Identity = 96%	Matches = 322	Mismatches = 7
Gaps = 4	Conservative Substitutions = 0	

```
     1550    1560    1570    1580    1590 X   1600    1610
CCCAAAGCTTTATCTGTCTTGACTTTTTAAAAAGTTTGGGGGGCAGATTCTGAATTGGCTAAAAAGACATGCA
                                             |||||||||||||||||||||
                                             TGAATTGGGCTAAAAGAC-TGCA
                                             X   10      20

     1620    1630    1640    1650    1660    1670    1680
TTTTTAAAACTAGCAACTCTTATTTCTTTCCTTTAAAAATACATAGCATTAAATCCCAAATCCTATTTAAAG
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TTTTTANAACTAGCAACTCTTATTTCTTTCCTTTAAAAANTACATAGCATTAAANCCCAAATCCTATTTAAAG
       30      40      50      60      70      80      90

     1690    1700    1710    1720    1730    1740    1750
ACCTGACAGCCTTGAGGANAGGTCACTACTACTGCATTATAGGACCTTCTGGGTGGTTCTGCTGTTACGTTTGAAGTC
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ACCTGACAGCCTTGAGGANAGGTCACTACTACTGCATTATAGGACCTTCTGGGTGGTTCTGCTGTTACNTTTGANANTC
     100    110      120      130      140      150      160

     1760    1770    1780    1790    1800    1810    1820    1830
TGACAATCCTTGAGANATCTTTGCATGCAGAGGAGGTAAGAGGTTATTGGATTTTTCACAGAGGAGGAAGAACACAGC
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TGACAATCCTTGANANATCTTTGCATGCAGAGGAGGTAAGAGGTTATTGGATTTTTCACAGAGGAGANANACACAGC
     170    180      190      200      210      220      230

     1840    1850    1860    1870    1880    1890
GCAG-AATGAA-GGGCCCAGGCTTACTGAGC-TGTCCAGTGGAGGGGCTCATGGGGTGGGACATGGAAAAAGAAGG
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GCAGAAAATGAAGGGGCCCAGGCTTACTGAGCTTGTCCACTGGATGGGGTGGGACATGGAAAAAGAAGG
     240    250      260      270      280      290      300

     1900    1910    1920 X   1930    1940    1950    1960    1970
CAGCCTAGGCCCCTGGGGAGGAGCCCAGTCCACTGAGCAAGCAAGGGACTGAGTGAGCCTTTTGCAGGAAAAGGCT
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CAGCCTAGGCCCCTGGGGAGCCCA
     310    320      330 X
```

A

Right column:

```
          310    320      330 X
CAGCCTAGGCCCCTGGGGAGGAGCCCA
||||||||||||||||||||||||||
CAGCCTAGGCCCTGGGGAGCCCA
          310    320    330 X
```

A

---

18. US-09-439-313-335 (1-2984)
   US-09-288-946-20 Sequence 207, Application US/09288946

   A

Sequence 207, Application US/09288946
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C7
CURRENT APPLICATION NUMBER: US/09/288,946
CURRENT FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 381
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 207
LENGTH: 332
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(332)
OTHER INFORMATION: n = A,T,C or G

Initial Score = 253	Optimized Score = 318	Significance = 1.84
Residue Identity = 96%	Matches = 322	Mismatches = 7
Gaps = 4	Conservative Substitutions = 0	

```
     1550    1560    1570    1580    1590 X   1600    1610
CCCAAAGCTTTATCTGTCTTGACTTTTTAAAAAGTTTGGGGGGCAGATTCTGAATTGGCTAAAAAGACATGCA
                                             |||||||||||||||||||||
                                             TGAATTGGGCTAAAAGAC-TGCA
                                             X   10      20

     1620    1630    1640    1650    1660    1670    1680
TTTTTAAAACTAGCAACTCTTATTTCTTTCCTTTAAAAATACATAGCATTAAATCCCAAATCCTATTTAAAG
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TTTTTANAACTAGCAACTCTTATTTCTTTCCTTTAAAAANTACATAGCATTAAANCCCAAATCCTATTTAAAG
       30      40      50      60      70      80      90

     1690    1700    1710    1720    1730    1740    1750
ACCTGACAGCCTTGAGGANAGGTCACTACTACTGCATTATAGGACCTTCTGGGTGGTTCTGCTGTTACGTTTGAAGTC
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ACCTGACAGCCTTGAGGANAGGTCACTACTACTGCATTATAGGACCTTCTGGGTGGTTCTGCTGTTACNTTTGANANTC
     100    110      120      130      140      150      160

     1760    1770    1780    1790    1800    1810    1820    1830
TGACAATCCTTGAGANATCTTTGCATGCAGAGGAGGTAAGAGGTTATTGGATTTTTCACAGAGGAGGAAGAACACAGC
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TGACAATCCTTGANANATCTTTGCATGCAGAGGAGGTAAGAGGTTATTGGATTTTTCACAGAGGAGANANACACAGC
     170    180      190      200      210      220      230

     1840    1850    1860    1870    1880    1890
GCAG-AATGAA-GGGCCCAGGCTTACTGAGC-TGTCCAGTGGAGGGGCTCATGGGGTGGGACATGGAAAAAGAAGG
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GCAGAAAATGAAGGGGCCCAGGCTTACTGAGCTTGTCCACTGGATGGGGTGGGACATGGAAAAAGAAGG
     240    250      260      270      280      290      300

     1900    1910    1920 X   1930    1940    1950    1960    1970
CAGCCTAGGCCCCTGGGGAGGAGCCCAGTCCACTGAGCAAGCAAGGGACTGAGTGAGCCTTTTGCAGGAAAAGGCT
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CAGCCTAGGCCCCTGGGGAGCCCA
     310    320      330 X
```

A

19. US-09-439-313-335 (1-2984)
US-09-352-616A-2 Sequence 295, Application US/0935261GA
GENERAL INFORMATION:
Patent No. 6395278
Sequence 295, Application US/0935261GA
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqui
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 295
LENGTH: 305
TYPE: DNA
ORGANISM: Homo sapien

Initial Score   =   215   Optimized Score   =   303   Significance = 1.50
Residue Identity =   98%   Matches   =   305   Mismatches   = 0
Gaps   =   4   Conservative Substitutions =   0

```
2460      2470      2480      2490      2500      2510      2520      2530
GCTCTTACATTTCTTTTAAAAATAAGCATTTAGTGCTCAGTCCCTACTGAGTACTTCTTTCTTCTCCCTCCTC
                                                       GTACTCTTTCTTCTCCCTCCTC
                                                       X        10        20

2540      2550      2560      2570      2580      2590      2600
TGAATTTAATTCTTTCAACTTGCAATTTGCAAGGATTACACATTTCACTGTGATTGTATATTGTTGTTGCAAAA
TGAATTTAATTCTTTCAACTTGCAATTTGCAAGGATTACACATTTCACTGTGATTGTATATTGTTGTTGC----
30        40        50        60        70        80        90

2610      2620      2630      2640      2650      2660      2670
AAAAAAAAAAAAGTGTCTTTGTTTGTTTTAAAATTACTTGGTTTGTTGAAATCCATCTTGCTTTTTCCCCATTGGAACTAG
AAAAAAAAAAAAGTGTCTTTGTTTGTTTTAAAATTACTTGGTTTGTTGAAATCCATCTTGCTTTTTCCCCATTGGAACTAG
100       110       120       130       140       150       160

2680      2690      2700      2710      2720      2730      2740
TCATTAACCCATCTCTGAAACTGGTAGAGAAAAACATCTGAAGAGCTAGTCATCAGCATCTCGACAGGTGAATTG
                                                                          170       180       190       200       210       220       230

2750      2760      2770      2780      2790      2800      2810
GATGGTTCTCAGAACCATTCACCCAGACAGCCTGTTTCTATCCTGTTTAATAAAATTAGTTTGGGTTCTCTA
GATGGTTCTCAGAACCATTCACCCAGACAGCCTGTTTCTATCCTGTTTAATAAAATTAGTTTGGGTTCTCT
240       250       260       270       280       290       300 X

2820      2830      2840      2850      2860
CATGCATAACAAACCCTGCTCCAATCTGTCACATAAAAGTCTGTGACTT
```

20. US-09-439-313-335 (1-2984)
US-09-232-149A-2 Sequence 295, Application US/0932214GA
GENERAL INFORMATION:
Patent No. 6465611
Sequence 295, Application US/0932214GA
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE

TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C6
CURRENT APPLICATION NUMBER: US/09/232,149A
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 295
LENGTH: 305
TYPE: DNA
ORGANISM: Homo sapien

Initial Score   =   215   Optimized Score   =   303   Significance = 1.50
Residue Identity =   98%   Matches   =   305   Mismatches   = 0
Gaps   =   4   Conservative Substitutions =   0

```
2460      2470      2480      2490      2500      2510      2520      2530
GCTCTTACATTTCTTTTAAAAATAAGCATTTAGTGCTCAGTCCCTACTGAGTACTTCTTTCTTCTCCCTCCTC
                                                       GTACTCTTTCTTCTCCCTCCTC
                                                       X        10        20

2540      2550      2560      2570      2580      2590      2600
TGAATTTAATTCTTTCAACTTGCAATTTGCAAGGATTACACATTTCACTGTGATTGTATATTGTTGTTGCAAAA
TGAATTTAATTCTTTCAACTTGCAATTTGCAAGGATTACACATTTCACTGTGATTGTATATTGTTGTTGC----
30        40        50        60        70        80        90

2610      2620      2630      2640      2650      2660      2670
AAAAAAAAAAAAGTGTCTTTGTTTGTTTTAAAATTACTTGGTTTGTTGAAATCCATCTTGCTTTTTCCCCATTGGAACTAG
AAAAAAAAAAAAGTGTCTTTGTTTGTTTTAAAATTACTTGGTTTGTTGAAATCCATCTTGCTTTTTCCCCATTGGAACTAG
100       110       120       130       140       150       160

2680      2690      2700      2710      2720      2730      2740
TCATTAACCCATCTCTGAAACTGGTAGAGAAAAACATCTGAAGAGCTAGTCATCAGCATCTCGACAGGTGAATTG
170       180       190       200       210       220       230

2750      2760      2770      2780      2790      2800      2810
GATGGTTCTCAGAACCATTCACCCAGACAGCCTGTTTCTATCCTGTTTAATAAAATTAGTTTGGGTTCTCTA
GATGGTTCTCAGAACCATTCACCCAGACAGCCTGTTTCTATCCTGTTTAATAAAATTAGTTTGGGTTCTCT
240       250       260       270       280       290       300 X

2820      2830      2840      2850      2860
CATGCATAACAAACCCTGCTCCAATCTGTCACATAAAAGTCTGTGACTT
```

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

> o/ o IntelliGenetics
> o <

Results file 700700-1X051080.res made by spaula on Wed 3 Sep 103 16:44:00-PDT.

Query sequence being compared:US-09-700-700-1 (1-1936)
Number of sequences searched: 19
Number of scores above cutoff: 19

Results of the initial comparison of US-09-700-700-1 (1-1936) with:
File : US09105470B.seq

SCORE 0   6   11   17   22   28   33   39   44   50
STDEV 0   11   17   22   28   33   39   44   50

S   0 -
E   -
R   10 -
O   -
F   -
      -
N 100 -
U   -
M   50 -
B   -
E   -
R   -
      -
O   -
F   10 -
      -
S   5 -
C   -
O   -
R   0 -
E
S

PARAMETERS

Similarity matrix   Unitary
Mismatch penalty   1
Gap penalty   1.00
Gap size penalty   0.33
Cutoff score   0
Randomization group   0

K-tuple   4
Joining penalty   30
Window size   500

SEARCH STATISTICS

Scores: Mean   Median   Standard Deviation
                   23   12   15.55

Times: CPU   Total Elapsed
                   00:00:00.01   00:00:00.00

Number of residues: 10987
Number of sequences searched: 19
Number of scores above cutoff: 19

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. US-09-105-470B-8	Sequence 8, Application U	3488	50	556	1.74	0
2. US-09-105-470B-2	Sequence 25, Application	3974	44	830	1.35	0
3. US-09-105-470B-2	Sequence 27, Application	415	43	182	1.29	0
4. US-09-105-470B-3	Sequence 3, Application U	705	42	308	1.22	0
5. US-09-105-470B-1	Sequence 1, Application U	705	42	308	1.22	0
6. US-09-105-470B-2	Sequence 29, Application	533	34	229	0.71	0
7. US-09-105-470B-3	Sequence 30, Application	318	33	152	0.64	0
8. US-09-105-470B-2	Sequence 26, Application	112	28	54	0.32	0
9. US-09-105-470B-2	Sequence 28, Application	507	25	219	0.13	0
10. US-09-105-470B-1	Sequence 16, Application	26	14	12	-0.71	0
11. US-09-105-470B-2	Sequence 20, Application	24	12	15	-0.77	0
12. US-09-105-470B-1	Sequence 24, Application	27	11	13	-0.77	0
13. US-09-105-470B-2	Sequence 15, Application	19	10	13	-0.84	0
14. US-09-105-470B-2	Sequence 22, Application	15	9	13	-0.90	0
15. US-09-105-470B-1	Sequence 19, Application	15	9	15	-0.90	0
16. US-09-105-470B-1	Sequence 18, Application	26	9	13	-0.90	0
17. US-09-105-470B-1	Sequence 17, Application	28	8	13	-0.96	0
18. US-09-105-470B-2	Sequence 23, Application	15	8	8	-0.96	0
19. US-09-105-470B-2	Sequence 21, Application	24	8	13	-0.96	0

1. US-09-700-700-1 (1-1936)
   US-09-105-470B-8 Sequence 8, Application US/09105470B

Initial Score   =   50   Optimized Score   =   556   Significance =   1.74
Residue Identity   =   47%   Matches   =   678   Mismatches   =   567
Gaps   =   187   Conservative Substitutions   =   0

```
                  X         10        20
                AATGGT-ATGCCAACTTAAGTA
TCCCTCCGGTGTGTCCAGGAGGAGAGTCCACTTATTTCTTTCCTGTCACTTCTCGATGAGCGCGCAGAAGCCC
2100      2110      2120      2130      2140 X  2150      2160

T-TTACAGGGTGGGCCCAAAATAGAA---CAAG-ATG-CACTGCGCTGTGATTTTAAGACAAGCTGTATAAACAGA
TCGTTTAGCGCAAGAGGGAATTAAAGCCCCAGAATGAGCCTTGCGTCCAAGACAGGGGCCT--AAGGAGG
2170      2180      2190      2200      2210      2220

ACTCCACTTGCAAGAGGGNGGGCCCGGGC-CAGGA-GAATCTCCGGCTTGTCCAAGCACAGGGCCCT--AAGGAGG
CCTCCTTGC-CCACCTGGATTCCTCAAACACCACGAAACGTCTTCACTTGGGTTCTTTGGATGAT-TCTTAGCA
2230      2240      2250      2260      2270      2280      2290      2300

GTCTCCACAACTGCTGCTAGGGGGCTGGTTGGCATTTTTTTATTAGTTAGGAAAG-TGGAAAGGCCTCTTCTCA-ACT
GCATTTTCCCTGC---CT--CCCT-CTCCCGCGCTCTCTCCAGCACACAGAAGAATCCCACATATAATTCT
2310      2320      2330      2340      2350      2360

TTTTTTCCCTTGGGCTGGGAGAAATTAGAATCA-GAA--GTTTC---CT-GGAGTT-TTCAGGCTATCATATAT
ACTAGACAGTAG---GGAGAAAGTTCAACCACACGAAACGTCTTCACTTGGGTTCTTTGGATGAT-TCTTAGCA
2370      2380      2390      2400      2410      2420      2430

ACTGTATCCTGAAAGGCAACAATAATTCTTC---CTTCCCTTCCTTTTAAAATTTGTTGTTCCTTTTTGCA---
AATGAATGCGTAA--TAAACATATTACTCACTCTTCACTCC--GGAGAGCTCCTTAGTCATGTGAATGAAAAG
2440      2450      2460      2470      2480      2490      2500

-GCAAT-TACTCAC---TAAAG---GGC--TTCATT---TTAGTCCAGATTTTTAGTTCTGGCTCGCACCTAACT
TGAAATGTATCCACGATGACAGTGGGCGTGTTGTTCACTCACTAAAGA-GATAAAGGGGTCGGATTGAATTCTCT
360       370       380       390       400       410
```

2. US-09-700-700-1 (1-1936)
US-09-105-470B-2 Sequence 25, Application US/09105470B

Initial Score = 44	Optimized Score = 830	Significance = 1.35
Residue Identity = 47%	Matches = 1040	Mismatches = 823
Gaps = 340	Conservative Substitutions =	

3. US-09-700-700-1 (1-1936)
   US-09-105-470B-2 Sequence 27, Application US/09105470B

Initial Score = 43   Optimized Score = 182   Significance = 1.29
Residue Identity = 47% Matches = 253   Mismatches = 158
Gaps = 122   Conservative Substitutions = X   = 0

4. US-09-700-700-1 (1-1936)
    US-09-105-470B-3 Sequence 3, Application US/09105470B

Initial Score = 42   Optimized Score = 308   Significance = 1.22
Residue Identity = 47% Matches = 415   Mismatches = 268
Gaps = 186   Conservative Substitutions = X   = 0

5. US-09-700-700-1 (1-1936)
US-09-105-470B-1 Sequence 1, Application US/09105470B

Initial Score	= 42	Optimized Score = 308	Significance = 1.22
Residue Identity	= 47%	Matches = 415	Mismatches = 268
Gaps	= 186	Conservative Substitutions = 0

```
              CTGAATTTAATTCTTTCAACTTGCAATTTGCAA

          630                640                650                660                670                680                690
CTGACAGCTTGAGGAGGTCACTCACTACTGCATTTATAGGACCTTCTGGTGGTTCTGCGTTGTTACGTTTGAAGTCTG
 |      |||||||   ||      |     |     ||         ||||||        |     |||||
CCG-CGGCCCGGGGAGG----CGAAAGC--GGAGGGGGGCC-----CGCGCGACCCCGTCCAAGCCGC
  20                30                40                50                60                70

          700                710                720                730                740                750                760
ACA-ATCCTTGAGGAATCTTTG-CATGCAGAGGAGAGGGTAAGAGGTGGATTTTCACAGAGGAAGAAGAC--ACA
  |||        |    ||||||   ||     ||    |   ||||    |||     |       |||||||
TCACGTTCCTTCATCCAGAGACATCCTGCCG-----GACCGGCGCGCCAGCGCGCAAGGCGGCGCGCACGAGCA
  80                90                100                110                120                130                140

          770                780                790                800                810                820                830
GCGCAGAATGA-AGGGCCAGGCTTACTGAGGCTG--TCCAGTG-GAGGGCTCATGGGTGGGGGACATGGGAAAAGA
   |||      ||    ||||   |     |||||    |||||    |       ||        |
GC--CAGA--GACAGCCGGA------CCCCGGAGCCCGGAGCCGCCAGAGCGCCAGAGC-CA---GAGGA--GG
  150                160                170                180                190
```

6. US-09-700-700-1 (1-1936)
US-09-105-470B-2 Sequence 29, Application US/09105470B

Initial Score	= 34	Optimized Score = 229	Significance = 0.71
Residue Identity	= 46%	Matches = 294	Mismatches = 223
Gaps	= 112	Conservative Substitutions = 0

7. US-09-700-700-1 (1-1936)
   US-09-105-470B-3 Sequence 30, Application US/09105470B

Initial Score = 33   Optimized Score = 152   Significance = 0.64
Residue Identity = 52%   Matches = 191   Mismatches = 115
Gaps = 61   Conservative Substitutions = 0

8. US-09-700-700-1 (1-1936)
   US-09-105-470B-2 Sequence 26, Application US/09105470B

Initial Score = 28   Optimized Score = 54   Significance = 0.32
Residue Identity = 50%   Matches = 62   Mismatches = 50
Gaps = 10   Conservative Substitutions = 0

9. US-09-700-700-1 (1-1936)
   US-09-105-470B-2 Sequence 28, Application US/09105470B

Initial Score = 25   Optimized Score = 219   Significance = 0.13
Residue Identity = 46%   Matches = 276   Mismatches = 221
Gaps = 96   Conservative Substitutions = 0

10. US-09-700-700-1 (1-1936)
    US-09-105-470B-1 Sequence 16, Application US/09105470B

Initial Score   =   12   Optimized Score   =   14   Significance = -0.71
Residue Identity   =   53%   Matches   =   14   Mismatches   =   12
Gaps   =   0   Conservative Substitutions   =   0

         460   470   480   490   500
ATAGC------------TGCGGTGC------------GGTAGCCCGGAC-CCACGTACTGCGAGCTCGAAAGC--GGG
                              ||| ||||| ||||||||||| |||
ATTGCCTATAATG--GGTCCCAAAAATGGGTAACCTAGACTTCAGAGAGAATGAGCAGAGAGAGAGAAAGGAGAAA
         980   990   1000   1010   1020   1030   1040 X

         1050   1060   1070   1080   1090
TCTGGGCTGTCCTTCCATTTTCATTCTGTTATCTTCAGGTGTGAGCTGG
||| X
GGCT
X

11. US-09-700-700-1 (1-1936)
    US-09-105-470B-2 Sequence 20, Application US/09105470B

Initial Score   =   11   Optimized Score   =   15   Significance = -0.77
Residue Identity   =   61%   Matches   =   16   Mismatches   =   8
Gaps   =   2   Conservative Substitutions   =   0

         820   830   840   850   860   870   880
ATGGGGTGGGACAATGGAAAAGAAGAAGGCAGCCTAGCCCCTGGGGACTCCACTGAGCAAGCAAGGGACTGA
                                                        |||| ||||||| |||
                                      CACTGCCCAGTCAAGTG--TTC
                                      X   10   20

12. US-09-700-700-1 (1-1936)
    US-09-105-470B-1 Sequence 15, Application US/09105470B

Initial Score   =   11   Optimized Score   =   13   Significance = -0.84
Residue Identity   =   48%   Matches   =   13   Mismatches   =   14
Gaps   =   0   Conservative Substitutions   =   0

         890   900   910   920   930   940
GTGAGCCTTTTCCAGGAGAAAAGGCTAAGAAAAAGGAAAAAACCATTCTAAAACACA
||| X
TTGA
X

13. US-09-700-700-1 (1-1936)

         1610   1620   1630   1640   1650
CCCATTGGAACTAGTCATTAACCCATCTCTGAACTGGTTAGAGAAAAACATCTGAAGA
|||| X
CGGAG
X

US-09-105-470B-2 Sequence 24, Application US/09105470B

Initial Score   =   10   Optimized Score   =   13   Significance = -0.84
Residue Identity   =   70%   Matches   =   14   Mismatches   =   5
Gaps   =   1   Conservative Substitutions   =   0

         170   180   190   200   210   220   230 X
ACTGCTGCTAGGGGGCTGTTGCATTTTTTATTAGTAGAAAAGTGGAAAAGGCCCTCTTCTCAACTTTTTTCCCTTT
                                                                    |||||||||||
                                                          CTCTAAT-GGCTTTTTTCTC
                                                          X   10

14. US-09-700-700-1 (1-1936)
    US-09-105-470B-2 Sequence 22, Application US/09105470B

Initial Score   =   9   Optimized Score   =   9   Significance = -0.90
Residue Identity   =   60%   Matches   =   9   Mismatches   =   6
Gaps   =   0   Conservative Substitutions   =   0

         1300   1310   1320   1330   1340   1350   1360
TTTCTGTGTTTGGGCTCCACATTGCAATGTTCCACGTGTCGTGCTGACACCGACCGAGTACTAGCCA
                                                        |||| |||||
                                              GCCGGATC----CTTACCCAAAA
                                              X   10   X

15. US-09-700-700-1 (1-1936)
    US-09-105-470B-1 Sequence 19, Application US/09105470B

Initial Score   =   9   Optimized Score   =   15   Significance = -0.90
Residue Identity   =   56%   Matches   =   17   Mismatches   =   9
Gaps   =   4   Conservative Substitutions   =   0

         70   80   90   100   110   120   130
AGACAAGCTGTATAAACAGAACTCCACTGCAAGAGAGGGNGGGCCCGGGCCAGGAGAGAAATCTCCGCTTGTCCAAGA
                                                                  |||| |||
                                                        GCCGGATC----CTTACCCAAAA
                                                        X   10   X

16. US-09-700-700-1 (1-1936)
    US-09-105-470B-1 Sequence 18, Application US/09105470B

Initial Score   =   9   Optimized Score   =   13   Significance = -0.90
Residue Identity   =   56%   Matches   =   17   Mismatches   =   9
Gaps   =   4   Conservative Substitutions   =   0

         150   160   170   180   190
CAGGGGCCTAAGGAGGAGGGTCCACACTGCTGTAGGGGGCTGTTGCATTTTTTTTATTAG
||||| X
GCTGGGGCT
20 X

         150   160   170   180   190
CAGGGGCCTAAGGAGGAGGGTCCACACTGCTGTAGGGGGCTGTTGCATTTTTTTTATTAG
||||| X
GCTGGGGCT
20 X

17. US-09-700-700-1 (1-1936)
US-09-105-470B-1 Sequence 17, Application US/0910547OB

Initial Score	=	9	Optimized Score	=	13	Significance	=	-0.90
Residue Identity	=	46%	Matches	=	13	Mismatches	=	15
Gaps	=	0	Conservative Substitutions	=	0			

```
      1530        1540        1550        1560        1570        1580        1590        1600
AATTGTGTTGCAGNGANGAAAAAAGAAAAAAAGTGTCTTTGTTTAAAATTACTTGGTTTTGTGAATCCATCTTGCTTTTTT
                                                              GCGGGAATCCCATGCTCAGGGGTT
                                                              X            10          20
```

```
      1610        1620        1630        1640        1650
CCCCAATTGGAACTAGTCATTAACCATCTCTGAACTGGTAGAAAAACATCTGAAGA
|  |
CCGGAG
X
```

18. US-09-700-700-1 (1-1936)
US-09-105-470B-2 Sequence 23, Application US/0910547OB

Initial Score	=	8	Optimized Score	=	8	Significance	=	-0.96
Residue Identity	=	53%	Matches	=	8	Mismatches	=	7
Gaps	=	0	Conservative Substitutions	=	0			

```
      1300        1310        1320        1330        1340        1350        1360
TTTCTGTGTTTGGGCTCCACATTGCAATGTTCAATGCCACGTGCTCGCTGACACCGACGGAGTACTAGCCA
                                                      ||||    ||||
                                                      ACACTACTTGGAGGC
                                                      X    10    X
```

```
      1370        1380        1390        1400
GCACAAAAGGCAGGGTAGCCTGAAATTGCTTTCTGCTCTTTACA
```

19. US-09-700-700-1 (1-1936)
US-09-105-470B-2 Sequence 21, Application US/0910547OB

Initial Score	=	8	Optimized Score	=	13	Significance	=	-0.96
Residue Identity	=	54%	Matches	=	13	Mismatches	=	11
Gaps	=	0	Conservative Substitutions	=	0			

```
      820         830         840         850         860   X 870         880
ATGGGTGGGACATGGAAAAGAAGGAGGCAGCCTAGGCCCTGGGGGAGCCCAGTCCACTGAGCAAGCAAGGGACTGA
                                                        |||||| || ||| ||||--|-
                                                        CACTGCCCAGTCACGTGTTCGT
                                                        X           10          20
```

```
      890         900         910         920         930
GTGAGCCTTTTGCAGGAAAAGGCTAAGAAAAAGGAAAAACCATTCTAAAACAC
GA
X
```

```
> O <
O| |O   Intelligenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file 020956_X_4399313.res made by spaila on Fri 12 Sep 103 15:35:26-PDT.

Query sequence being compared:US-09-020-956-53 (1-484)
Number of sequences searched:                    1
Number of scores above cutoff:                   1

Results of the initial comparison of US-09-020-956-53 (1-484) with:
     File : 439313-335mod.seq


100-


N
U  50-
M
B
E
R
       10-
O
F
       5-
S
E
Q  0-
U     0---+----+----+----+----+----+----+----+----+----+----+
E     0    6   11   17   23   28   34   40   45   51
N
C  SCORE
E  STDEV

SCORE 0    6   11   17   23   28   34   40   45   51
STDEV                                              *


                      PARAMETERS

Similarity matrix   Unitary    1
Mismatch penalty    1.00       Joining penalty          30
Gap penalty         0.33       Window size             484
Gap size penalty    0
Cutoff score        0
Randomization group 0


                  SEARCH STATISTICS

Scores:       Mean      Median    Standard Deviation
              51        0         0.00

Times:                           Total Elapsed
              CPU                 00:00:00.00
              00:00:00.00

Number of residues:              2984
Number of sequences searched:       1
Number of scores above cutoff:      1

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

Sequence Name | Description | | Init. | Opt. |
---|---|---|---|---|---
 | | Length | Score | Score | Sig. | Frame

1. US-09-439-313-33 Sequence 335, Application US/09439313   2984   51   223   0.00   0

1. US-09-020-956-53 (1-484)
   US-09-439-313-33 Sequence 335, Application US/09439313

Sequence 335, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqui
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 335
LENGTH: 2984
TYPE: DNA
ORGANISM: Homo sapien

```
Initial Score      =   51    Optimized Score      =   223    Significance =   0.00
Residue Identity   =   48%   Matches              =   266    Mismatches   =   207
Gaps               =   73    Conservative Substitutions
```

```
                10                    20
         X                    X    ACATAATTTAGCAGGGCTAATT
CAGCTTGAGAAGTCACTTACTCGCATTTATAGGACCTTCTGGGTTGGGTTCTGCGTTACGTTTG-AAGTTGACA
   1700      1710      1720      1730      1740  X 1750      1760

                30                    40                    50                    60                    70                    80
A-CCATAAGATGCTATTTATTTAANAGG-TNTATGA--TCTGAG-TATTAACAGTTGCTGCTGAAGTTTG-GTATT
   1770      1780      1790      1800      1810      1820      1830

                90                    100                   110                   120                   130                   140                   150
ATCCTTGAGAAATCTTGCATGCAGAGAGGGGGTAAGAGAGGACTGAGTGAGCCCTTTTTG-CAGGAAAAAGGCTAAG
   1910      1920      1930      1940      1950      1960      1970

TTTATGCAGCATTTTCTTTTGCTTTGAATAAACTACTACAGAACCCTT--AAGGACACTGAAAAATTAGTAAGT
   1840      1850      1860      1870      1880      1890      1900

ATGAAGGGCCA--GGCTTACTGAGCTG-T-CCAGTGAGGGGGCTCATGGGGTGGGCATGGAAAAGAAGAGGCAGC
   1840      1850      1860      1870      1880      1890      1900

AAAG----TTCAGA-AACATT-AGCTGCTCAATCAAATCTCTACATAACACTATAGTAAAACGTTAAA
   160       170       180       190       200       210       220

CTAGGGCCTTGGGGGACCCAGTCCACTGAGCAAGCACGAGGGACTGAGTGAGCCCTTTTTG-CAGGAAAAGGCTAAG
   1910      1920      1930      1940      1950      1960      1970

AAAAAGTGTTGA--AATCTT---GCACTAGTATANACCGCTCC---TGTCAGGATAANACTGCTT-TGGAACA
   230       240       250       260       270       280

AANAAG-GAAAACCCATTCTAAAACACAACAAGAAAACTG-TCCAAATCGCTTTGGGAACTGTGTTTAATGCCTA
   1980      1990      2000      2010      2020      2030      2040

GAAAAGGG----AAAA--ANCAGCTTTGANTTTCTTTGTG-CTGA--TANGAGGAAAGGCTGAAT-TACCT-
   290       300       310       320       330       340

TAATGGGTGCCCCAAAAATGGGTAACCTAGA-CTTCAGAGAGGAGAATGAGCGAGAGAGGAGAAATCTCGGCTG
```

```
       2050      2060      2070      2080      2090      2100      2110

       350       360       370       380            390            400
  TG-TTGCCTCTCCCTAATGAT-TGGCAGGT---CNGGTA---------AATNCCAAAACATATTCCAACTC
  | |||||||| |||||||||| |||||||     ||||||        ||||||||||||||||||||||
  TCCTTCCATTTTCATTCTGTTATCTCAGGTGAGCTGGTAGAGGGGGAGACATTAGAAAAAAATGAAACAACAA
       2120      2130      2140      2150      2160      2170      2180

       410       420       430       440            450            460
  AACACTT-CTT-T---TTCCNCGTA--NCT-TGANTCTGTGTATTCCAGGA--NCAGGCCGGATGGAATGGGC
  |||| |  | | |    |||| |||    |  ||||||||||||||||||    ||||||||||||||||||
  AACAATTACTAAATGAGGGTACGCTGAGGCCTGGGGAGTCTCTCTTGACTCCACTACTTAATTCCG-TTTAGTGAG-
       2190      2200      2210      2220      2230      2240      2250

       470       480      x
  CAGCCCNCGGATGTTCCANT
  | ||         ||||
  AAACCTTTCAATTTTCTTTTATTAGAAAGGGCCCAGCTTACTGTTGGTGGTGCAAAAATTGCCAACAATAAGTTAA
       2260      2270      2280      2290      2300      2310      2320
```